



Db	401	GLULENLAARGTGLEUGLUTTRPROLYTYGLEVALSERHVSERRPROASPLGYLY	420
OY	1261	AACAGCTCGGCCAAGGTGACACTGCACACAGC-----AGCGAGCCAAAGGG	1311
Db	421	ASMSERRGYSINSGRIANSCYSSERRSERGLYGLYSERCUYLAASNL	440
OY	1312	ACGGGGTGGAGGCTGGGGCGCGCTGGCTGGCGAGCGCTACATACCTCCCTAC	1371
Db	441	THRIYLEUGLLEUGLYGLYPROSERLEUARGSERALATYTLERRSERLEUYT	460
OY	1372	TTGCGACTACAGACCTCACACGGTGGCTTGGCAAGTGGCGGCCAAACGGACAC	1431
Db	461	PHENALEUSERRSERLEUTINSEVALGYPHEGLYASNAVALSERLAASNHASPHR	480
OY	1432	GAGAGATCTTCTCCATCTGCACACATGCTATGGGGCCCTGATGACAGCGGTGTTT	1491
Db	481	GLUYSLERPESSERLECYSTHMETLEULLEUYLALEUMETHSLAVALALPHE	500
OY	1492	GGGAACGTGACGGCCATCATCGAGGCTGATGACGCCCGCGCTTGTGACACAGCCG	1551
Db	501	GLYASNAVALTHALALERLEOINRYMETLYRLAARGHPRHELEUYTHLSERRAT	520
OY	1552	ACGGCGACCTCGGACATCCGATCCGATCCGATCCGATCCGATCCGATCCGATCCG	1611
Db	521	THIRYASPLEAARGASPRYTLERAGTLERHSHARGTLEROLYSPROLEUYSGINATG	540
OY	1612	ATGCTGGATCTTCCAGGCACTCGGGCGGTGAACAATGGCAATCGACACAGACTG	1671
Db	541	MELLEUGLUTYR-PHEGLNALATHTRPRALVALASNAAGLYTLASPTHTHGLILEU	560
OY	1672	CTGCAGAGCTCCCTGACAGAGCTGGCGCGAGACATCGGCATGACCTCACAGAGGTC	1731
Db	561	LEUGLINSERLEUPROASPRGLUEURLAARGALASPRLEALAMETHLSLENNLSYGLVAL	580
OY	1732	CTGCAGCTGCCATGTTTGGAGGGCGGACCCCGGCTGGCTGGCGACTCTTGCGC	1791
Db	581	LEUGLINSERPROLEUPHEGLUALAALASERLAGLYCYSLAENDARGALALEUSERRLEUALA	600
OY	1792	CTGGCGCGCGCTTCTGCACAGCGGCGAGTACCTTCATCCACCAAGGAGTCCCTGGAG	1851
Db	601	LEUARGPROALARPHECYSTHTRPROGLYGLYTLLEUINLEHISGLNGLYASRALALEUGLN	620
OY	1852	GCCCTACTTCTTCTGCTGCTGCTGCTCCATGGAGGTGCTMAAGGTTGGACGCTGGCTGCC	1911
Db	621	ALALEUYRPHIVALCYSSERGLYSERMETGLIVALLEUYSGLYTHRYVALLEUALA	640
OY	1912	ATCTAGGGAAGGCGACACTGATGGCTGTGAGCTGGCCCGGAGAGAGTGTAAAG	1971
Db	641	ILEUGLYLSGLYASPRLEUINLEGLYCYSGLJLEUPROGLNARGGLINGVALVALYS	660
OY	1972	GCCAAATGCCAAGCTGAAAGGGGCTGACCTAGCTGCTGCAAGTGTGTGCAGTGGCTGGC	2031
Db	661	ALASNAALASPRVALYSGLYLEUTHTRYCYSTVALLEUGINCYSLAUGLINSLEUINLEUALAGLY	680
OY	2032	CTGCACAGACGCTTGGCTGCTTACCCGAGTTTGCCCGCGCTTCACTGGCTGGCTCCGA	2091
Db	681	LENNHLSERLEUINLEUALALEUYTRPROGLUPHEALARPROARGPHESETRARGLYLEUARG	700
OY	2092	GGGAGACTAGCTACAACTGGGTGCTGGGAGAGGCTCTGCAGAGGTTGGACACAGCTCC	2151
Db	701	GLYGLJLEUSERTYASNLNGLYALAGLYVALSERLAAGLVALASPTHSERSET	720
OY	2152	CTGAGCGGAGACATACCTTATGTCACAGCTGGGAGGGAAGAGACAGATGGGAGACAG	2211
Db	721	LEUSERTGLYASPNHTRLEUMETSETRHLEUGLINSGLUYLSGLUTHASPRGLYGLN	740
OY	2212	GGCGCCAGGCTCTCCCGACCCCGATATGAGCCCTCAGCGCCCTGCTCCCTGGC	2271
Db	741	GLYHSHRTHLESERPROALARPROALASPRGLUPROSERPROLEUENUSERRPROGLY	760
OY	2272	TGCACCTCTCATCTCAGCTGGCAGCTGATCCGATCCGATCCGATCCGATCCGAGCT	2331

Dp 761 CysThrSerSerSerSerAlaAlaValSerLeuLeuSerProArgThrAlaProArgPro 780

QY 2332 GCTAGTGGTGCAGAGGAGGAGCCGAGGAGGAGGAGGCTTTGAAGCTTAGGCTGGCCCC 2391

Dp 781 ArgLeuArgLeuArgLeuArgProSerArgAlaGlyValLeuLeuSerProGluAlaGlyPro 800

QY 2392 TCTGCTCCCCCAGCGGCCCTAGAGAGGGGCTTCAGGCTGCCCCCATGGCATGGAATGGCC 2451

Dp 801 SerAlaHisProArgThrLeuAspGlyLeuGlnLeuProMetProThrPheValPro 820

QY 2452 CCAGATGTAGCCCCCAGGCTAGTAGATGGCATTTAGAGAGGCTGTGGCTGGAGCACGCC 2511

Dp 821 ProAspLeuSerProArgValValAspGlyLeuGluAspGlyCysGlySerAspGlnHis 840

QY 2512 AAGTCTCTTCCGGGTGGGCCAGTGTGGCCCCGGAATGTAGCAGAGGCCCTCCCTGGA 2571

Dp 841 LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly 860

QY 2572 CCAGAGAGCGGCTGCTCACTGTTCCCATGGGCCCCAGCAGGAGGACACAGACACA 2631

Dp 861 ThrGluSerGlyLeuLeuThrValProLeuValProSerGluAlaArgAsnThrAspThr 880

QY 2632 CTGGACAGCTTCGGCAGAGCGGTGACAGAGCTGTACAGAGCGGTGCTGCAGATCGGGAA 2691

Dp 881 LeuAspLysLeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGlu 900

QY 2692 GGACGTGCACTACTTCGCCAGAGCTGTGCAGCTTGTGGCGGCCCCAGAGAGGGTCCG 2751

Dp 901 GlyLeuGlnSerLeuArgGlnAlaValGlnLeuLeuValProGlnGlyGluGln 920

QY 2752 TGCCCTCGGGATGGGGAGAGGGCCCTGCCACACAGACACTCCGGGCTTCGAGGCT 2811

Dp 921 CysProArgValSerGlyGluGlyProCysProAlaThrAlaSerGlyLeuLeuGlnPro 940

QY 2812 CTGTGTGTGACACTGGGGCATCTCTACTGCTGTGAGCGCCCAAGCTGACTGTGCTTG 2871

Dp 941 LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu 960

QY 2872 AGTGGAGCTTGCCCCACCTCGTCCGGGG---CTGCTGCCCTAATGGACACCTGGCCC 2928

Dp 961 SerIleThrThrProHisProArgProGluHisProProLeuMetAlaProThrPro 980

QY 2929 TGGGGTCCCCCAGCGTCTCAGAGCTCCCTGGCCCTGAGCCACAGACTTTCGGAGCCTCC 2988

Dp 981 ThrIleProProAlaSerGlnSerSerProThrProArgAlaThrAlaLeuThrPheSer 1000

QY 2989 ACCTCAGACTCAGAGGCCCTGCTCTAGAGACCTCTGCTGAGCCAGACACCTGCC 3048

Dp 1001 ThrSerAspSerIleProProGlySerGlyAspLeuCysSerGluProSerThrProAla 1020

QY 3049 TCCCTCTCTCTTTCAGAGAGGGGCTAGAGACTGGGCCCCGAGAGCCTGTGAGCAGGCT 3108

Dp 1021 SerProProProProGluGluGlyAlaThrGlyThrProAlaProValSerGlnAla 1040

QY 3109 GAGGCTACAGACACTGAGAGAGCCCCACACAGAGGTACAGGGGCCCTGGCCTTGGCCGGAC 3168

Dp 1041 GluAlaThrSerThrGlyLupProProGlySerGlyAlaArgAlaLeuProThrPasp 1060

QY 3169 CCCACAGCGCTGGAGATGGTGTATTGGCTGCATGGCTGCTGAGCAGACAGTCAGTGGACC 3228

Dp 1061 ProHisSerLeuGluMetValLeuIleGlyCysHisGlyProGlySerValGlnThrPthr 1080

QY 3229 CAGGAAGAAGGACAGGGGCTC 3349

Dp 1081 GlnGluGluGluGlyThrGlyVal 1087

J. Physiol. 511, 675-682, 1998  
A:Title: Cloning of a mammalian elk potassium channel gene and EAG mRNA distribution  
A:Reference number: Z18731, MVID:98382545, PMID:9714851  
A:Accession: T17367  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1102 <SH1>  
A:Cross-references: EMBL:AF061957; NID:93659689; PID:93659690; PIDN:AA661520.1  
A:Genetics:  
A:Gene: elk1  
C:Function:  
A:Description: may play a role in the sympathetic nervous system  
C:Keywords: potassium channel

Alignment Scores:

File#	NO.	6.98e+123	Length:	1107
Score:		2515.00	Matches:	551
Percent Similarity:		62.00%	Conservative:	149
Best Local Similarity:		48.80%	Mismatches:	295
Query Match:		41.30%	Indels:	134
DB:		2	Gaps:	24

1-3252) x T17367 (1-1102)

[illegible]

Db	569	ThrsrPhecySaIaPrOglIyGluTyrLeuLeuAylGlnIyAspAlaLeuGlnAlaIle	588
Qy	1858	TACTTTGTCTGCTTGGCTCCATGGAGGTGCTCAGAGGTGGACCGCTGCTGGCATCTTA	1917
Db	589	TyrPheValIcysSerIySerMetGluValLeuIleuAspSerMetValLeuAlaIleu	608
Qy	1918	GGGAAGGGCGACGTATCGGCTGTGAGCTGCTCCCGGGGAGCAGCTGGTAAAGCCAT	1977
Db	609	GlyIlySglAspLeuIleGlyAlaAsnLeuSerIleuAspAlaIleuIlyThrAsn	628
Qy	1978	GCCGACGTGAAGGGGCTGACCTACTGCTGCTTCAGTGTCTGACAGCTGGCTGGCCGAC	2037
Db	629	AlaAspValIySaIaLeuThrTyrCysAspLeuGlnIyIleLeuIySglLeuPhe	648
Qy	2038	GACAGCTTTGGCTGATCCCGAGCTTTGGCCCCGGCTTCAAGTGGTGGCCCTCCAGGGAG	2097
Db	649	GluValLeuGlnLeuTyrProGluTyrAlaIlySAspLeuGlnIyIleLeuIlyThrAsn	668
Qy	2098	CTCAGCTACACCTGGGTCTGG-----GGAGGCTCT	2130
Db	669	LeuThrTyrAsnLeuAlaGlnIyIleGlnIySerAspValIleSerAylLeuSerAsnIyS	688
Qy	2131	GCAAGAGTGCACACAGCTCCCTGAGCGGCGACATACCTTATGTCACAGCTG-----	2184
Db	689	SerThrValProGlnAlaGluProIySglAsnGlnSerIleuIySArgLeuProSer	708
Qy	2185	-----GAGAGAGAGACAGATGGGGAGCAGGGCCCCACGGTCTCCCGACGCCA	2235
Db	709	IleValGlnAspGlnLeuGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyThrThrSerLeuSerPro	728
Qy	2236	GCATGATGAGCTCCAGCCCCCTGCTGCTCCCTGGCTGACACTCTCTCACTCCAGCTGCC	2295
Db	729	IleTyrThrArgIySerSerIleSerIlySerIlySglIySerIlySerIySglIyS	748
Qy	2296	AACTGCTATCCCACTGCA-----ACAGCACCC-----CGGCT-----CGT	2334
Db	749	LeuGlnLeuSerLeuIySglLeuThrSerGlyThrValProPheIlySerProIleArg	768
Qy	2335	CTAGTGGCAGAGGAGCGACGAGGCGAGGGGCTTTGAGCTGAGCTGAGCTGGCCCTCT	2394
Db	769	ValSerSerAlaAsnSerPro-----LysThrIySglGlnIyAlaAspProPro	784
Qy	2395	GCTCCCCACGGGCTTACAG-----GGGCTACGGCTGCCCCCATGCCATGAGAT	2445
Db	785	AsnIlySglIyThrArgIySglIyAsnLeuIyValGlnLeuIySerLeuIyThrAla	804
Qy	2446	GTGCCCGAGATCTGAGCCCCAGGCTGATGATGCAATTAAACGGCTGGCTGCGAC	2505
Db	805	GlyThrProGlnLeuSerProArgIleValAspIyIleGlnAspGlnAspIyAsnSerSerGln	824
Qy	2506	CAGCCCAAG-----TCTCTTTCCGGCTGGGCGACGTCTGCCCGGATGATGACACAGCCCC	2562
Db	825	GlnThrGlnThrPheAspPheIySerGlnIleArgProGlnProAlaGlyIleSerPro	844
Qy	2563	TCCCTGACACAG-----AGGCGCTGCTCACTGTTCCCATGGGCCACAGAG	2613
Db	845	SerLeuGlnIyGlnSerIleGlyAlaAlaPheLeuPheIle-----Lys	859
Qy	2614	GCAAGAAACA-----CACACTGACATCTCGGAGCGGTGACAGAGCTGTACAG	2670
Db	860	AlaGlnIyThrIySglGlnIleAsnIySglLeuAsnSerGlnValThrThrLeuThrGln	879
Qy	2671	CAGGTGCTGACATGCGGAGAGACTGACATCTCCGACAGGCTGTGACACTGTGCTGT	2730
Db	880	GlnValSerIleuGlnIyAspMetArgSerIleMetGlnLeuGlnIyAsnIleu	899
Qy	2731	GGCGCCACAGGGAGGCTCCGTGCTCCGCGCATGGGAGAGGGCGCGGCCAGCCAGC	2790
Db	900	SerProGlnIyProSerGlnPheCysSerLeuIlySProIlySerIleCysProSerArg	919
Qy	2791	ACCTCCGGGCTTCTGACGCTCTGTGTGAGACACTGGGCGACCTCCACACTGCTGAG	2850
Db	920	GlnSerPheGlnThrArg-----ValSerTyrSerAlaIlySglProCysLeuIlyS	936

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OY 2851 CCCCGAGT-----GGCTGTCTTGTAGTGAGACTGGCCCGAC 2889
Db 937 LeuGlnAlaAsnGlyAlaHisLeuThrHisGlyAsnValThrSerIleTrp-----954
OY 2890 CCTCGTCGGGGGCTCCCTCCATGGACACCTGGGCGTCCCGACGGCTCTAG 2949
Db 955 -----SerValAspProSerLeuValGlySerAsnProGlnArgThrGlnAlaHisGlu 972
OY 2950 AGCTCCCGC----- 2958
Db 973 GlnSerProValAspSerGluLeuHisHisSerProAsnLeuAlaTyrSerProSerHis 992
OY 2959 -----TGCGCTCGACCCACA 2973
Db 993 CysGlnValIleGlnGluGlyHisLeuGlnPheLeuAlaGlyCysIleSerProHisSerAsp 1012
OY 2974 GCTTTCGGACCTCCACCTCAGACTCAGAGCCCGCTGCCTCAGAGACCTGCTCTAG 3033
Db 1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrLeuSerSerSerValCysSerSer 1032
OY 3034 CCCAGCACCT-----GCCTCCCTCTCTCTCTGTGAGAGGGGCTAGACT--- 3081
Db 1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGluGlnGlySerIleThrHis 1052
OY 3082 GGGCCCGCAGAGCTGTGAGCCAGCTGAGGCTACAGACTGAGAGAGCCCGACAGGG 3141
Db 1053 GlyProValSerSerPheSerLeu-----GluAsnLeuProGly 1065
OY 3142 TCAGGGGGGCTGGCTTGGCTGGGAC 3168
Db 1066 Ser-----TrpAsp 1068

RESULT 3
T31354
probable potassium channel elk chain 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R:Engelard, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.
submitted to the EMBL Data Library, July 1998
A:Description: Identification of three rat potassium channel genes homologous to D. melo
A:Reference number: 220983
A:Accession: T31354
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1017 <EMBL>
A:Cross-references: EMBL:AJ007628; NID:e1329997; PID:e1329998; PIDN:CA07587.1
C:Genetics:
A:Gene: elk1
C:Keywords: potassium channel

Alignment Scores:
Pred. No.: 5.65e-119 Length: 1017
Score: 2439.50 Matches: 532
Percent Similarity: 60.00% Conservative: 131
Best Local Similarity: 48.14% Mismatches: 244
Query Match: 40.06% Indels: 198
Gaps: 23

US-09-965-830-1_COPY_6_3257 (1-3252) x T31354 (1-1017)
OY 1 ATGCGCGCATGCGGGGCTCTCTGGCGCTCAGAAACCTTCTGTGACACCATGCTAG 60
Db 1 MelProValMetCysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20
OY 61 CGCTTCAGCGCAGCAGCAGTAATCTGTCTGTGGCAGCCGCGGCGGCTCTTC 120
Db 21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnAlaGlnGlyProArgGlyPhe 40
OY 121 CCCGTGTACTACTGTCTGTGCTTCTGTGACTCAGCGGCTTCCCGGCTGAGCTC 180

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Db 41 ProIleValTyrCysSerAspGlyPheCysGluLeuThrGlyTyrGlyArgThrGlnVal 60
OY 181 ATCAGCGGGGCTGTGGCTCTCTCTCTCTTATGGCCAGACACCACTGAGCTGTCCGC 240
Db 61 MetGlnHisThrCysSerCysArgPheLeuTyrGlyProGlnThrSerGluProAlaLeu 80
OY 241 CAACAGATCCGCAAGGCCCTGGACGAGCACACAGAGACTCAAGGCTAGGCTGCTGAC 300
Db 81 GlnArgLeuGlnLysAlaLeuGlnGlyHisGlnGlnHisArgAlaGlnIleCysPheTyr 100
OY 301 CGAAGAGCGGCTCCCTGTGTGTCTCTGTGATGTATGATCCATAAGATGAGAA 360
Db 101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetPheProIleLysAsnGluLeu 120
OY 361 GGGAGGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db 121 GlyGluValValLeuPheLeuPheSerPheLysAspIleSerGlnSerGlyGlyProGly 140
OY 421 -----GCCCCGACAGATGGAAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
Db 141 LeuGlySerProGlyIleHisGlyLysAspAsnAsnHisGlnAsnSerLeuGlyArg--- 159
OY 460 CGATATGCGCGGCGCAGATCCAAAGCTTCAATGCCAACCGCGCGGACCGGCGCTG 519
Db 160 -----ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal 176
OY 520 CTCTACCACTGTCCGGGACCTGTGACAGAGAGCCAGAGAGAGAGAGAGAGAGAGAG 579
Db 177 LeuHisArgLeuThrGlnHisPheGlyArgArgAspGlnGlnSerValLysAlaAsnSer 196
OY 580 GGGGTGTTGGGGAACCAACTGGCTGTAGTACAAGTAGCGGCGGACCGGAGTCG 639
Db 197 AsnValPheGluProLysProSerValProGluTyrLysValAlaIleSerValGlyLys 216
OY 640 CCTCTACCTGTGTGACATGTGGGCGCTGAGAGCCAGCTGGAGTTCATCTCTCTC 699
Db 217 ArgCysLeuLeuHisTyrSerIleProLysAlaValTrpAspGlyLeuLeuLeu 236
OY 700 GCCACACTATGAGGCTGACAGTGCCTTACAGCCTGTGTGTGACAGACAGCGGAG 759
Db 237 AlaThrPheTyrValAlaValThrValProTyrAsnValLysPheAlaGlyAspAsp 256
OY 760 CCGAGTCCGCGCGCGCGCGCGCGCGCTGTGACCTGGCGCTGGAGGCTCTTCATC 819
Db 257 ThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPheIle 276
OY 820 CTTGACATGTGTGTAATTCCTTACACATTCGTGTCCAAAGTGGGCGAGGTGTGT 879
Db 277 LeuAspIleIleLeuAsnPheArgThrThrTyrValSerIleSerGlyGlnValAlaSer 296
OY 880 GCCCAAGTCCATTTGCTCCACTACGTACACCACTGTGCTCTGTGATGCATCGCA 939
Db 297 AlaProArgSerIleGlyLeuHisTyrLeuAlaThrThrPhePheValAspLeuIleAla 316
OY 940 GCGTGCCTTGTGACTGTATACATGCTTCAAGGTCAACGTACTCTCGGGCCCATCTG 999
Db 317 AlaLeuProPheAspLeuTyrValPheAsnIleThrValThrSerLeuValHisLeu 336
OY 1000 CTGAAGAGGTGGCGCTGTGCGCTGTGCGGCTTCCCGGCTGAGACCGGTACTCG 1059
Db 337 LeuLysThrValArgLeuLeuArgLeuLeuValGlnValGlnGlnValArgTyrSer 356
OY 1060 CAGTACAGCGCGGTGTGTACACTGCTCAATGCGCTGTGGCTGTGGCGAGCTG 1119
Db 357 GlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHisTrp 376
OY 1120 GTCCGCTGCTGTGTTTACATTGGCCAGGAGATCGAGAGAGAGAGAGAGAGAGAG 1179
Db 377 MetAlaCysValTrpTyrValIleGlyArgArgGluMetGlnAlaAsnAspProLeuLeu 396
OY 1180 CCTAGATGTGGCTGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1239
Db 397 TrpAspIleGlyThrLeuHisGlnLeuGlyLysArgGlnGlnGlnGlnGlnGlnGlnGln 413

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C:Accession: T13168  
R:Warnke, J.W.; Ganetzky, B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994  
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals  
A:Reference number: A54953; M0ID:94211879; PMID:8159766  
A:Accession: T13168  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1284 <WAW>  
A:Cross-references: EMBL:U04246; NID:g487735; PID:g487736; PIDN:AAA62472.1  
C:Genetics:  
A:Gene: elk  
A:Cross-references: FlyBase:FBgn0011589  
A:Map position: 2R

Alignment Scores:	
Pred. No.:	4 44e-91
Score:	1501.00
Percent Similarity:	55.85%
Best Local Similarity:	40.77%
Query Match:	31.23%
DB:	2
	1280
Length:	455
Matches:	146
Conservative:	273
Mismatches:	242
Indels:	31
Gaps:	21

03 03-503-630-1\_COPY\_b\_3257 (1-3252) x TL3168 (1-1284)

QY 1 AGCGGGGCATCGGGGGCTCTCGGCGCTCAGAACACCTCTCGGACACATCGGTACG 60  
 Db 1 MetProAlaArgLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20  
 QY 61 CGCTTCGAGCGGAGCGACAGTAACATTCCGTGCGGCGAACGCCAGGTGCGGGGCTCTTC 120  
 Db 21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39  
 QY 121 CCGGTGTCTACTGCTGTGATGGCTTCTGTGACCTCAGCGGCTTCTCCGGGCTGAGTTC 180  
 Db 40 ProIleValIlyrCysSerAspGlyPheValAspIleuThrGlyTyrSerArgIleGlnIle 59  
 QY 181 ATGCAGCGGGGCTGTGCTGCTCTCCCTCTTATGGCGCAGACACCAGTGAAGCTCGTCCG 240  
 Db 60 MetGlnLysGlyCysSerCysHisPheLeuTyrGlyProAspThrLysGlnIuHisLys 79  
 QY 241 CACACAGTCCGCAAGGCCCTGAGACGACACAAAGGTTCAAGGCTGAGACTGATCTGTAC 300  
 Db 80 GlnGlnIleGlnLysSerLeuSerAsnLysMetGluLeuLysLysGlnIleValIlePheTyr 99  
 QY 301 CGGAGAGCGGGCTCCCGTCTGTGCTGTCTCGATGTGATACCCATACGAATGAGAA 360  
 Db 100 LysLysGlnIuGlyLapProPheTrpCysLeuPheAspIleValProIleLysAsnGlnLys 119  
 QY 361 GGGAGGTGGCTCTCTTCCTAGTCTCTCACAGGACATCAGCAAGCAAG----- 411  
 Db 120 ArgAspValValLeuPheLeuAlaSerHisLysAspIleThrHisThrLysMetLeuGln 139  
 QY 411 ----- 411  
 Db 140 MetAsnValAsnGlnIuLysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla 159  
 QY 412 -----AACCGAGG 420  
 Db 160 ArgPheArgAlaGlySerSerAsnAlaGlyMetLeuGlyLeuGlyLysLeuProGlyLeuGly 179  
 QY 421 GGCCCC-----GACAGATGGAAGAGAGACGAGGCGTGGCGCGCGCGATGTGGCCGG 471  
 Db 180 GlyProAlaIaSerAspLysAspThrGlyAlaGlyGlnGlyLysAsnAsnLeuAspValPro 199  
 QY 472 GCACAGATCCAAAGCTTCAATGACCAACCGCGGGAGGCGGGCGGTCTTACCACTG 531  
 Db 200 Ala-----GlyCysAsnMetGlyArgAlaArgSerArgAlaValLeuTyrGlnLeu 216  
 QY 532 TCCGGGCACTGCAGAACGAGCCCAAGGCG-----AAGCAGACATCAATGAAGGG----- 582  
 Db 217 SerGlyHisTyrLysProGlnLysGlyGlyValLysThrLysLeuLysLeuGlyAsnAsn 236

[illegible]





QY	757	GAGCCAGTGC-----	-----GCCCGGCGCCCGCCAGCGTGTGACCTGGCC	8
Db	439	GLYProProAlaThrIleGlyCysGLYIYrAlaCysGlnProLeuAlaValValAspLeuIle		4
QY	802	GTCAGAGCTCTTCAATCCCTTGACATGTGGCGAATTTCGCTACCAATCTGTGTCCAG		8
Db	459	ValAspIleMetIleThrIleValAspIleLeuIleAsnProIleAsnProIleArgThrThrIYValAsnAla		4
QY	862	TCCGGCCAGGTGGTGTGTTTGCACCAAGATCATTTGCTCCACATACAGTACCACCTGGTC		9
Db	479	AsnGlnGluValValSerHisProGlnArgIleAlaValAlaHisTYrPheIYsgLYrPhe		4
QY	922	CTGCTGGATGTATGCGACAGCGCTGGCCCTTTGACCTGTACATATGCTTCACAGTCAAGTCAAGT		9
Db	499	LeuIleAspMetValAlaAlaIleProPheAspLeuLeu-----		51
QY	982	TACTTGGGGG-----	-----CATGCTGTAAGACGTGGCGCTGGCGG	10
Db	512	IlePheGlySerGlySerIleGluIleLeuIleGlyLeuIYsThrAlaArgLeuLeuArg		53
QY	1024	CTGCTGCGCTGCTCTCCCGCGCTGGACCGGATCCGCGAGTACAGCGCCGTGGTGCACA		10
Db	532	LeuValAlaArgValAlaAlaGlyIYsLeuAspArgIYsSerIYrGlyAlaAlaValLeuPhe		55
QY	1084	CTGCTCATGCGCGGTGTGGTCCCTCTGTCGCGACATCGGGTGGCCGCGCTGGTTTACAT		11
Db	552	LeuLeuMetCysThrProPheAlaLeuIleAlaHisTyrPheuAlaCysIleTyrAlaIle		57
QY	1144	GCCACGCGGGAGATCGAGACAGCAGGAATCCGAGCTGCTGACATGTGGCTGGTGCAGAG		12
Db	572	GlyIYsMetGluGlnProHisMetAspSer-----	ArgIleGlyTyrPheuHisAsn	58
QY	1204	CTGCGCCGCGACATCGAGAGATCCCTCTACTCTGTGGCGGAGCCAGCTGAGAGAAC		12
Db	589	LeuGlyAspIleGlnIleGlyIYsProTYr-----	Asn	59
QY	1264	AGCTCCGCGCAGAGTGCACACTCAGCAGACAGACAGAGCCAACGGGAGCGGCTGGAG		13
Db	599	SerSerGly-----	-----	60
QY	1324	CTGTGGGCGCGCGTGGCTGGCGACGCGCTACATCACTCCCTACTTGGCTACAC		13
Db	602	---LeuGlyIYrProSerIleIYsAspIYrValIThrAlaLeuTYrPheThrPheSer		62
QY	1384	AGCCTACACAGCGTGGGCTTGGCAACGTGTCCGCCAACAGCAGCAGCAGAGAAATGTC		14
Db	621	SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGlyIYsIlePhe		64
QY	1444	TCCATCTGCACATGCTACTACGGCGCCCTGATGCACGCGGTGTGTGGGAAGCTGAC		15
Db	641	SerIleCysValMetLeuIleGlySerIleuMetTYrAlaSerIlePheGlyAsnValSer		66
QY	1504	GCCATCATTCAGCGCATGTACGGCGCGCGCTTGTGACACACGCGCAGCGGACCTG		16
Db	661	AlaIleIleGlnArgLeuTYrSerGlyIYrAlaAlaTYrHisThrGlnMetLeuArgVal		68
QY	1564	CCGCACTACATCCGATCCACACCGTATCCCAAGCCCTCAAGAGAGGCAATGCTGAGATAC		16
Db	681	ArgGluPheIleAlaArgPheHisGlnIleProAsnProLeuIYrGlnArgLeuIYrGlu		70
QY	1624	TTCGAGGCGCACCTGGCGGCGTGAACATGGCATGAGACACACCGATGTGTGAGAGCGTC		16
Db	701	PheGlnHisAlaIYrSerTYrTYrAsnGlyIleAspMetAlaAlaValLeuIYsGlyPhe		72
QY	1684	CTGACAGCATGGCGCGAGACATCCGATGCACTGCAACAGAGAGTCTGTGAG---CTG		17
Db	721	ProGlnIYsLeuGlnAlaAspIleCysLeuHisIleuAsnArgSerLeuLeuIYsHisCys		74
QY	1741	CCACTGTTTGAGGCGCGCACCGCGCTGCGCGGCGCACTGTCTGTGCGCTCGCGCC		18
Db	741	LysProPheArgGlyAlaThrIYsGlyCysLeuAlaGlnAlaLeuAlaMetIYsPheIYrThr		76

D	761	ThrHisAlaProProGlyAspThrLeuValHisAlaGlyAspLeuThrAlaLeuI	780
Q	1861	TTTTGTCTGCTCTGGCTCCATGAGGAGGTCACAGGAGGCGACCGCTGCTCCATCTAGCG	1920
D	781	PheIleSerArgIleSerIleGluIleLeuAlaGlyAspValValAlaIleLeuGly	800
Q	1921	AAGGCGACCTGATCGGCTGTGACTGCTGCCCGCGGAGCAGGCTGTAAAGCCAAATGCC	1980
D	801	LysAsnAspIlePheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsnGly	820
Q	1981	GAGCTGAAGGCGGCTGAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040
D	821	AspValAlaGalaLeuThrTyrCysAspLeuHisLysIleHisArgAspLeuLeuGlu	840
Q	2041	AGCCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2100
D	841	ValLeuAspMetTyrProGluPheSerAspHisPheIlePheSerLeu-----GluIle	858
Q	2101	AGCTTAAACCTG-----CGTCTGGGGAGAGCTGTCGACAGAGTGGAC	2142
D	859	ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerThrGluLeuGlu	878
Q	2143	ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2202
D	879	GlyGlyPheSerArgIleArgIleArgIleArgIleArgIleArgIleArgIleArgIle	898
Q	2203	GGGAGCAGAGGCGCCACAGCTGCCACAGCCCGAGCTGATGAGCCCTCCAGCCCTCTG	2262
D	899	ThrGluGlu-----	901
Q	2263	TCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2322
D	902	ProGlyGluValSerIle-----LeuGlyProGlyArgIleGly	914
Q	2323	CCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2382
D	915	AlaGlyPro-----SerSerArgIleArgProGlyGlyProIleGlyLeuSerProSer	932
Q	2383	GCTGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2418
D	933	SerGlyProSerSerProGlySerSerGlyAspGluGlyProGlyArgSerSerPro	952
Q	2419	CTACGCTG-----CCGCCATCCATGGAATGTGCCCGCCAGATCTGAGCCCC	2466
D	953	LeuArgIleValProPheSerSerProArgProGlyGluProProGlyGlyGluPro	972
Q	2467	AGGAGTACATGATGATGAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2514
D	973	LeuMetGluAspCysGluLysSerSerAspIleCysAsnProLeuSerGlyAlaPhe	991
Q	2515	-----TTCCTCTTC-----CGCGTGGCGCAGTCT	2538
D	992	SerGlyValSerAsnIlePheSerPheThrPheLysPheArgIleArgGlnTyrGlnGlu	1011
Q	2539	GCGCCGAGATGTAGCAGCAGCCCTCCCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2595
D	1012	LeuProArgCys-----ProIleProIleProIleProIleProIleProIlePro	1026
Q	2596	-----CCCATGGGGCCAGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2634
D	1027	LeuSerSerProGlyArgArgProArgIleAspValGluSerArg-----Leu	1042
Q	2635	GACACAGCTTCGCGAGCGCTGACAGAGCTGTCAGCAGCAGCTG-----CTGCAGATCGGGA	2691
D	1043	AspAlaLeuGlnArgGlnLeuAsnArgLeuGlnIleThrArgLeuSerAlaAspMetalThr	1062
Q	2692	GAGCTGAGTCACTTGGCAGCGCTGTGCACTGTGCTGGCGCCCGCAGGAGAGGTCCG	2751
D	1063	ValLeuGlnLeuLeuGlnArgGlnMetThrLeu-----	1073
Q	2752	TTCGCTGGGATCGGAGAGGCGGCGTCCGACCGACGACCTCGGGCTTCTGAGCT	2811

Dd	1074	-----ValProProlAlaIyrSerAla--	1080
QY	2812	CMTGTGTGGACACTGGGCGATCCTTACTAGCTGCAGAGCCCAAGCTGGCTGTCTTG	2871
			:::
Dd	1081	---ValThrThnProGlyProGlyProthrSerThrSerProleuLeuProVaISerPr	1099
QY	2872	AGTGGACTGTGGGCCAACCCCTGCTCGGGGCGCTCTCCCCCTCATGGCACCCCGGCCCTGG	2931
		:::	
Dd	1099	oleu-----ProthrLeuthrLeuasPserLeuSerGln-----	1110
QY	2932	GGTCCCCCAAGCGTC-----AGAGCTCCCGCTGCAGCCACAGCTTTCTGG	2982
		:::	:::
Dd	1111	-ValSerGlnPheMetIaLcysGlnGluLeuProProGly--AlaProGluLeuProGl	1129
QY	2983	ACCTCCACCTCAGACTCAGAGAGCCCGCTGCTCAGAGAGACTGCTGTGAGAGCCAGACACC	3042
		:::	:::
Dd	1129	nGlnGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlnAlaLeuThrSerGlnPr	1149
QY	3043	CCTG 3046	
Dd	1149	oleu 1150	

RESULT 6  
A40853  
potassium channel protein eag - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 24-Sep-1998  
C:Accession: A40853  
R:Warrick, J.; Drysdale, R.; Ganetzky, B.  
Science 257, 1560-1562, 1991  
A:Title: A distinct potassium channel polypeptide encoded by the *Drosophila* eag locus  
A:Reference number: A40853; MIMD:91262635; PMID:1840699  
A:Accession: A40853  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1174 <MAR>  
A:Cross-references: GB:M61157; NID:q157311; PID:q157312  
C:Genetics:  
A:Gene: FlyBase:eag  
A:Cross-references: FlyBase:FBgn0000535  
C:Keywords: transmembrane protein

Alignment Scores:	
Pred. No.:	1,296-64
Score:	1390.00
Percent Similarity:	47.57%
Best Local Similarity:	31.55%
Query Match:	22.83%
DB:	2
Length:	1174
Matches:	300
Conservative:	198
Mismatches:	398
Indels:	250
Gaps:	42

NS-09-965-830-1\_COPY\_6\_3257 (1-3252) X AA0853 (1-1174)

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QY      1  ATGCCG---GCCATGCGGGGCTCCTGCGCTCAGAACACCTTCTCGACACACACCTGCT  57
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1  MetProGlyGlyArgArgGlyYleuValAlaIleProIleAsnThrPheLeuGluAsnIleIle  20
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      58  ACGCGCTTCGACGC---ACGCACAGTAATTCGTGCGGGCCAGCGCCACGCGGAGGCGG  114
      |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|
Db      21  ArgArgSerAsnSerGlnProAspSerSerPheLeuLeuAlaAsnAlaGlnIleValAsp  40
      |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|  |||  ::|
QY      115  CTCCTCCCGCTGACTACTGCTCTCATGCTCTGTGTCACCTCAGCGGCTTCTCCGGGCT  174
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      41  ---PheIleValIleValIlyrCysAsnGluSerPheCysIlyIleSerGlyTYrAsnAlaGala  59
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      175  GAGGTATGACGACGGGGCTGT-----GCTGCTCCTCTCCCTTATGGGGCCAGACACAGT  228
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      60  GluValMetClnIlySerCysArgTYrValCysGlyPheMetTYrGlyGluLeuThrAsp  79
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      229  GAGCTGCTCCGCCCAACAGATCCGCAGCGGCTCGACAGCAGACACAGGACTCAGGCTGAG  288
      ::|  ::|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      80  LysGluThrValGlyIleValGluGluTYrThrLeuGluAsnGlnGlnAspGlnPheGlu  99
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      289  CTGATCTCTGATACCGGAGAGCGGGCTC-----  315

```





D 175 GlyIuSnValHISLysHisSerArgLeuAlaGluValLeuGlnLeuGlySerAspIle 194  
Q 586 TTGGGGGAAACCAACTTGGCTGAGTACAAGTACGCCGACCGGACGAGTGGCTTTC 645  
D 195 -----LeuProGlnIleTyrGlnGlnIleAlaProIlePheProIleHis 208  
Q 646 ATCTGTGACCTGTGGGGGCACTGAGAGCCACTGGGATGGCTTCATCTGCTGCCACA 705  
D 209 ILeIleuHisTyrCysValPheIleHisThrThrAspTrpIleIleuIleLeuThr 228  
Q 706 CTCATGTGGCTGTCCATGTGGCTTACAGGTGTGTGTGACACAGACGGGAGCCAGT 765  
D 229 PheTyrThrAlaIleLeuValProTyrAsnValSerPheIleTyr-----ArgGlnAsn 247  
Q 766 GCGCGCGGGCGCGCCAGCTGTGTGACCTGGCGGTGGAGCCCTTCATCTTGAC 825  
D 248 ValAlaIleTyr-----LeuValValAspSerIleValAlaPheIleValAsp 264  
Q 826 ATGTGTGTGATTTCCGTACACATTCGTGTCCAGTCCGGGAGGTGTGGCCCA 885  
D 265 ILeValIleuAsnPheHisThrThrPheValGlyProAlaIleGluValIleSerAspPro 284  
Q 886 AAGTCATTTGGCTCCACACAGTACACACCTGTGCTGTGTGATGTACAGAGCGCTG 945  
D 285 LysLeuIleArgMetAsnTyrIleuLysThrTrpPheValIleAspLeuLeuSerCysLeu 304  
Q 946 CCTTTGACCTGTACATGCTTCAG-----GTCAAGCTGATTCGGG 990  
D 305 ProTyrAspValIleAsnAlaPheGlnAsnValAspGluGlyIleSerSerLeuPheSer 324  
Q 991 GCGCATCTGTGACAGAGGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGAC 1050  
D 325 Ser-----LeuLysValValArgLeuLeuArgLeuGlyArgValAlaIleArgLysLeuAsp 342  
Q 1051 CGGTACTGCACTACAGCGCGCTGTGTGACACTGTGTGATGGCTGTGTGCTGTGCTGCTC 1110  
D 343 HisTyrIleGluTyrGlyAlaAlaValLeuValLeuLeuValCysValAlaPheGlyLeuAla 362  
Q 1111 GCGACGTGGGTCGCTGTGCTGTGTGTATGACATGGCAGCGGAGATGACAGACAGCA 1170  
D 363 AlaHisThrMetAlaCysIleTyrPheSerIleGlyAspTyrGluIlePheAspIleAsp 382  
Q 1171 TCCGAG---CTGCTGTGATTTGGCTGTGCTGTGACAGAGCTGGCCCGGACGTGAGACTGCC 1227  
D 383 ThrIleThrIleArgAsnAsnSerTrpLeuTyrGlnLeuAlaIleuAspIleGlyThrPro 402  
Q 1228 TACTACCTGTGTGGCCGGAGCGACAGCTGGAGGAAACAGCTCCGGCAGAGTACAACTGC 1287  
D 403 TyrGlnPhe-----AsnGlySerGlySerGlyLysTyrGlu----- 414  
Q 1288 AGCAGCAGCAGCGAGCGCAACGAGGAGCGGTGAGCTGTGGGGCGCCCTGCTGCC 1347  
D 415 -----GlyGlyProSerLysAsn 420  
Q 1348 AGGCGCTACATCACTCTCTTACTTGTGACATGACAGCTCAGCAGCTGAGGCTGGCTGCC 1407  
D 421 SerValTyrIleSerSerLeuTyrPheThrMetThrSerLeuThrSerValGlyPheIle 1440  
Q 1408 AAGGTGCGCCGAACAGCAGCAGGAGAAATCTTGTCACTGTGACACATGCTATGCTGCGC 1467  
D 441 AsnIleIleArgSerThrAspIleGluTyrIlePheAlaValAlaIleMetMetIleGly 460  
Q 1468 GCGCTGATGACCGCGGGGTGGTGGAGAGTACAGCCCATCACTCAGCCATGATGACGC 1527  
D 461 SerLeuLeuTyrAlaThrIlePheGlyAsnValThrThrIlePheGlnGlnMetTyrAla 480  
Q 1528 CCGCGCTTCTGTACACAGCGCCAGCGCGGACCTGGCGGACATCAACATCCCATCCACGT 1587  
D 481 AsnThrAsnArgTyrHisGlnMetLeuAsnSerValAlaArgAspPheLeuLysLeuTyrGln 500  
Q 1588 ATCCCAACAGCCCTCAGACAGCGCATGTGTGAGTACTTCCAGGCGACCTGGGCGGAGAC 1647  
D 501 ValProLysGlyLeuSerGlyIleValMetAspTyrIleValSerThrTrpSerMetSer 520  
  
Q 1648 AATGCATGCACACACCGAGCTGTGTGACAGACCTCTCCCTGAGAGTGGCGAGACATC 1707  
D 521 ArgGlyIleAspThrGluValValLeuGlnIleCysProLysAspMetArgAlaAspIle 540  
Q 1708 GGCATGCACCTGCACACAGAGAGTCTGT---CAGTGCACCTGTGTGAGCGCGCAGCCGC 1764  
D 541 CysValHisIleAsnArgLysValPheIleGlnHisProAlaPheArgLeuAlaSerAsp 560  
Q 1765 GAGTCCGCGGGGAGACTGTCTGTGCGCTGTGCGCGCGCTGTGTGACAGCGCGGAGTAC 1824  
D 561 GlyCysLeuArgAlaLeuAlaMetGluPheGlnThrValHisCysAlaProGlyAspLeu 580  
Q 1825 CTCATCCACCAAGAGATGAGCTGTGAGCCCTGTACTTGTGTGTGTGTGTGTGTGTGAG 1884  
D 581 IleTyrHisAlaGlyGluSerValAspSerLeuLysPheValIleSerGlySerLeuGlu 600  
Q 1885 GTGCTCAAGAGGTGACACCGTGTGTGCTGTGCTGTGAGGAGGCGACGTGAGTGTGAG 1944  
D 601 ValIleGlnAspArgGluValAlaIleLeuGlyLysGlyAspValPheGlyAspVal 620  
Q 1945 CTGCGCGCGGGGAGCAGGTGTGTAAGGCCATGTCCGAGTGAAGGGGTGAGTACTGC 2004  
D 621 PheTrpLysGluAlaThrIleuAlaGlnSerCysAlaAsnValArgAlaLeuThrTyrCys 640  
Q 2005 GTCTGTGAGTGTGTGACGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2064  
D 641 AspLeuHisValIleLysArgAspAlaLeuGlnIleValLeuGluPheTyrThrAlaPhe 660  
Q 2065 GCGCCGCGCTGTGAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2109  
D 661 SerHisSerPheSerArgAsnLeu-----IleLeuThrTyrAsnLeuArgLysArgIle 678  
Q 2109 ----- 2109  
D 679 ValPheArgLysIleSerAspValLysArgGluGluGlnIleArgMetLysArgLysAsn 698  
Q 2109 ----- 2109  
D 699 GluAlaProLeuIleLeuProProAsnHisProValArgArgLeuPheGlnArgPheArg 718  
Q 2110 -----CTGGTGTGTGCGGAGCTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTG 2151  
D 719 GlnGlnLysGlnAlaArgLeuAlaIleGluAlaGluArgGlyLysArgAspLeuAspSerLeu 738  
Q 2152 CTGACGCGGACAAATACCTTATGTGC---ACCTGAGAGAGAGAGAGAGAGAGTGGAG 2208  
D 739 ValGluLysGlyAsnAlaLeuThrAspHisThrSerAlaAsnHisSerLeuValLysAla 758  
Q 2209 CAGGCGCCAGCGGTGTCCAGCCCGGAGCTGTGAGAGCTGTGAGCCCTGTGCTGCCCT 2268  
D 759 SerValValThrValArgGluSerProAlaThrProValSerPheGlnAlaIleAsp 777  
Q 2269 GAGTGCACCTGTATCTGTGACTGTGCAAGCTGTGATCCCAAGTGCAGACAGCAGCCCGG 2328  
D 778 ---ThrSerThrValSerAspHisAlaLeuHisAlaProGlySerGlyCysLeuGly 796  
Q 2329 CCTGTGTGAGTGTGACAGAGGAGGAGCGCAGGCGAGG----- 2367  
D 797 ProLysAlaGlyGlyLysAspProAlaLysArgLysGlyTyrAlaAlaGlyPheLysAspAla 816  
Q 2368 -----GCTTGAAGCTGTGAGCTGTGCGCTGTGCTGCC 2400  
D 817 CysGlyLysGlyLysAspTyrAsnLysValSerLysAlaGluSerMetGluThrLeuPro 836  
Q 2401 CCAAGGCGCTTAGAGGGGTACAGGCTGCCCGCCATGCCATGGAATGTGCCCAAGATCTG 2460  
D 837 GluArgThr-----LysAla 841  
Q 2461 AGCCCAAGGAGTGTGATGTGATGAAGAGCGGTGTGTGCTGTGAGCAGCCAGCTGTCT 2520  
D 842 SerGlyGluAlaThrLeuLysLysThrAspSerCysAspSerGlyIleThrLysSerAsp 861

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QY 2521 TTCGGGTGGGCAAGTCTGGCCCGAATGTAGACAGACCCCTCCCTGACAGAGAGC 2580
    |||...|||
Db 862 LeuValGluAspAsnValValy-----GluAlaArgSerProGlnAspArgSer 877
QY 2581 GGCGTCTACT-----GTTCCCATGGGCGCCAGCGAGCA 2616
    |||...|||
Db 878 ProIleuAlaGluValLysHisSerPheTyProIleProGluGlnThrLeuGlnAla 897
QY 2617 AGGACACAGACACTGGACAGACTTCGGCAGCGGTGACAGCTGTACAGAGAGGTG 2676
    |||...|||
Db 898 ThrValLeuGluValLysHisGluLeuLysGluAspLLeuLysAlaLeuAsnAlaLysMet 917
QY 2677 CTCACATCGCGGAGAGAGACTGCAGTCACTTCGCGAGGCTGTGAGTTCGTGGCGCC 2736
    |||...|||
Db 918 ThrSerLLeuLysGluLeuSerGluLLeuArgLLeuMet----- 932
QY 2737 CACAGGAGGAGTCCGTCCTCGGCGATCGGAGAGGCGCGTCCAGCCAGCAGCTCC 2796
    |||...|||
Db 933 -----SerArgLysSerSerGlnSerProGlnAspThrCys 944
QY 2797 GGGCTCTGCAGCCT 2811
    |||...|||
Db 945 GluValSerArgPro 949

RESULT 8
148912
potassium channel subunit - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 148912
R:Marmke, J.W.; Ganetzky, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.
A:Reference number: A54953; MUID:94211879; PMID:8159766
A:Accession: 148912
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-989 <RES>
A:Cross-references: EMBL:U04294; NID:9487739; PIDN:AAA62474.1; PID:9487740
C:Genetics:
A:Gene: m-eag

Alignment Scores:
Pred. No.: 1,16e-63 Length: 989
Score: 1371.50 Matches: 341
Percent Similarity: 50.14% Conservative: 189
Best Local Similarity: 32.26% Mismatches: 310
Query Match: 22.52% Indels: 217
DB: Gaps: 31

US-09-965-830-1_COPY_6_3257 (1-3252) x 148912 (1-989)
QY 13 CGGGGCTCTGGGCGCTCAGAACACTTCCTGACACATCGTACGGCTTCAGCGC 72
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Db 8 ArgGlyLeuValAlaProGlnAsnThrPheLeuGluAsnIleValAlaArgArgSerAsnAsp 27
QY 73 ACGCACAGTAACCTCTGTGTGGGCAAGCCAGAGTGGCGGCTCTCCCGCTGTAC 132
    |||...|||
Db 28 Thr-----AsnPheValLeuGluAsnAlaGlnIleValAsp---TrpProIleValTy 44
QY 133 TCGCTGATGGCTCTGTGTGACCTCAGCGGCTTCCTCCGGCTGAGCTCAGCAGCGGGC 192
    |||...|||
Db 45 SerAsnAspLysPheCysLysLeuSerGlyTyrHisArgAlaGluValMetGlnLysSer 64
QY 193 TGTGCTGTCTCTCTCTTATTTGGGCGCAGACACAGTACGTCGTCGCCCAAGATCCGC 252
    |||...|||
Db 65 SerAlaLysSerPheMetTyrGlyLLeuThrAspLysPheValGluValArg 84
QY 253 AAGGCCCTGACAGCAGCAAGGATCAAGGCTGATCTGTATCCGGAAGAGCGGG 312
    |||...|||
Db 85 GlnThrPheGluAsnTyrGluMetAsnSerPheGluIleLeuMetTyrLysLysAsnArg 104
QY 313 CTCGGTTCGTGCTCTCTGATGTATACCATTAAGATGAGAAAGGAGGAGTGCT 372

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Db 105 ThrProValThrPhePheValLysIleAlaProIleArgGlnGluGlnAspLysValVal 124
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QY 373 CTCCTCTACTCTCTCAAGACATCAGCAGAAACCAAGACGAGGGGCCCGCAGCA 432
    |||...|||
Db 125 LeuPheLeuLysThrPheSerAspIleThrAlaPheLysGlnProIleGluAspArgSer 144
QY 433 TGAAGAGACAGAGTGTGGCCGG---CGCCGATATGGCGGACAGATCCAAAGGCTTC 489
    |||...|||
Db 145 CysLys-----GlyTrpGlyLysPheAlaArgLeuThrArgAlaLeuThrSer----- 160
QY 490 AATGCCAACCGGCGGCGGAGTCCGCTCTACCACTGATCCGGGCGACCTGACAGAG 549
    |||...|||
Db 161 -----SerArgLysValLeuGlnGlnIleuAlaProSerValGlnLys 174
QY 550 ---CAGCCCAAGGCGCAACAC-----AGCTCATTAAGGGGTG 585
    |||...|||
Db 175 GlyLysAsnValHisLysHisSerArgLeuAlaGluValLeuGlnLeuGlySerAspIle 194
QY 586 TTGGGGAAGAAACAAACTGCTGAGTACAAATAGCCGCGCATCCGGAATGCCCTTC 645
    |||...|||
Db 195 -----LeuProGlnTyrLysGlnGluAlaProLysThrProPheHis 208
QY 646 ATCTGTGTGCACTGTGGGCGCATAGAGCCACGTGGAGTGGCTTCACTGCTGCGACA 705
    |||...|||
Db 209 IleIleuHisTyrCysValPheLysThrThrTrpAspTrpIleIleLeuIleLeuThr 228
QY 706 CTCATGTGGCTGTGCTGAGTGGCTTACAGCGTGTGTGACACAGCAGGAGGCCAGT 765
    |||...|||
Db 229 PheTyrThrAlaIleLeuValProTyrAsnValSerPheLysThr---ArgLysAsnAsn 247
QY 766 GCGGCGCGCGCGCCCGCAGCGCTGTGACAGTGGCGGTGAGAGTCTTCACTGTGAC 825
    |||...|||
Db 248 ValAlaIlePhe-----LeuValAlaAspSerIleValAspValIlePheLeuValAsp 264
QY 826 ATTGTGTGATTTCCGTAACACATTCGTGTCAAGTGGCGGCGAGTGGTGTTCGCCCA 885
    |||...|||
Db 265 IleValLeuAsnPheHisThrThrPheValGlyProAlaGlyLysValIleSerAspPro 284
QY 886 AAGTCCATTTGCTCCACATCTCAGCAGACACACCTGCTCCGTGATGATCCAGAGCTG 945
    |||...|||
Db 285 LysLeuIleArgMetAsnTyrLeuLysThrThrPheValIleLysPheLeuLysSerLys 304
QY 946 CCTTTGACCTGCTACATGCTTC-----AAGTCACCTGTACTTGGG--- 990
    |||...|||
Db 305 ProTyrAspValIleAsnAlaPheGluAsnValAspGluValSerAlaPheMetGlyAsp 324
QY 990 ----- 990
Db 325 ProGlyLysIleGlyPheAlaAspGlnIleProProLeuGlnGluArgLysSerGln 344
QY 991 -----GCCATGTGTGAGACAGGTGGCGCTGCTGCGCTGCGCCCTG 1035
    |||...|||
Db 345 GlyIleSerSerLeuPheSerSerLeuLysValValArgLeuLeuArgLysValArgVal 364
QY 1036 CTTCGCGGCTGACCGGATCACTGCTGACAGGCGCGTGTGTCGACATGCTATGCC 1095
    |||...|||
Db 365 AlaArgLysLeuAspHisTyrIleGlyTyrGlyAlaAlaValIleValLeuValCys 384
QY 1096 GTGTTCGCTGCTGCTGCGGACCTGGGCTGCTGCTGCTGCTTACATGTCAGCGGAG 1155
    |||...|||
Db 385 ValPheGlyLeuAlaAlaHisThrPheAlaCysIleThrPyrSerIleGlyAspTyrGlu 404
QY 1156 ATCGAGAGCAGCGCAATCCGAG---CTGCTGAGATTTGCTGCTGCTGCTGAGAGTGGCCGC 1212
    |||...|||
Db 405 IlePheAspGluAspThrLysThrIleArgAsnAsnSerThrPheLysValLeuAlaLeu 424
QY 1213 CGACTGAGACTCCCTACTACTGCTGTGGCGGAGGCCAGCTGAGAGGAGACAGTCCGGC 1272
    |||...|||
Db 425 AspIleGlyThrProTyrGlnPhe-----AsnGlySerGlySerIle 438
QY 1273 CAGAGTCAACATCTCAGCAGCAGCAGCAGGCGCAACGAGGAGCGGCTGAGACTGCTGGGC 1332
    |||...|||

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Db 439 LysTrpGlu-----GLY 442
OY 1333 GGCGCCGCTGGCGAGCGCCCTACATCCCTCTACTTGCAGTCCAGGCTTACC 1392
Db 443 GlyProSerLysAsnSerValTyrIleSerSerLeuTyrPheThrMetThrSerLeuThr 462
OY 1393 AGCGTGGGCTGGCGAAGCTGTCCGCCAACAGCAGCAGCAGAGAGATCTTCTCATCTGC 1452
Db 463 SerValGlyPheGlyAsnIleAlaProSerThrAspIleGluLysIlePheAlaValAla 482
OY 1453 ACCATGCTCATCGCGCCCTGATGACGCGGTGGTGTGGTGGAGTGGAGTGGAGTGGAGT 1512
Db 483 IleMetMetIleGlySerLeuLeuTyrAlaThrIlePheGlyAsnValThrThrIlePhe 502
OY 1513 CAGCGCATGACCGCCGCGCTTCTGTACACGCGCGCAGCGCGCAGCTGGCGCATAC 1572
Db 503 GlnGlnMetTyrAlaAsnThrAsnThrAsnThrAsnThrAsnThrAsnThrAsnThrAsn 522
OY 1573 ATCCGATCCACCGCTATCCCGCCCGCTTCTGTACACGCGCGCAGCTGGCGCATAC 1632
Db 523 LeuLysLeuTyrGlnValProLysGlyLeuSerGlnAlaGlyValMetAspTyrIleValSer 542
OY 1633 ACCTGGGCGGTGACAAATGGCATGACACACCGAGTGTGTGAGAGCTCCCTCCAGCAG 1692
Db 543 ThrTrpSerMetSerArgGlyIleAspThrGluLysValLeuGlnIleCysProLysAsp 562
OY 1693 CTGGCGCCAGACATCGCGCATCGCATCGACAGAGAGCTCTG--CAGCTGCCATCTTT 1749
Db 563 MetArgAlaAspIleCysValHisLeuAsnArgLysValPheLysGlnHisProAlaPhe 582
OY 1750 GAGCGCGCAGCGCGCTGCTGCGCGCATCTGTCTGCGCGCCCGCCGCTTCTGC 1809
Db 583 ArgLeuAlaSerAspGlyCysLeuAlaGlnAlaLeuAlaMetGlnPheGlnThrValHisCys 602
OY 1810 ACCCGCGCGCATCTACATCCACAGAGCGAGTCCCTGAGCGCCCTCTACTTGTCTGC 1869
Db 603 AlaProGlyAspLeuIleTyrHisAlaGlyLysValAspSerLeuCysPheValVal 622
OY 1870 TCTGGCTCATGAGTGTGCTCAAGGGTGGCGACCTGCTCCATCTCCAGAGAGCGGAC 1929
Db 623 SerGlySerLeuGlnValIleGlnAspAspGlnValAlaIleLeuGlnLysGlyAsp 642
OY 1930 CTGATGCGCTGTGAGCTGCGCGCGCGCGAGCAGAGTGTAAAGCCATGCCAGCTGAAG 1989
Db 643 ValPheGlyAspValPheThrLysGlnAlaThrLeuAlaGlnSerCysAlaAsnValArg 662
OY 1990 GGGCTGACGCTACTGCTCTCTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2049
Db 663 AlaLeuThrTyrCysAspLeuHisValIleLysAlaGlyAspAlaLeuGlnLysValLeuGln 682
OY 2050 CTGTACCCCGAGTGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2109
Db 683 PheTyrThrAlaPheSerHisSerPheSerArgAsnLeu-----IleLeuThrTyrAsn 700
OY 2109 ----- 2109
Db 701 LeuArgLysArgIleValPheArgLysIleSerAspValLysArgGlnGlnGlnGlnGln 720
OY 2109 ----- 2109
Db 721 MetLysArgLysAsnGlnAlaProLeuIleLeuProAspHisProValArgArgLeu 740
OY 2110 -----CTGGTGTCTGGGAGAGCTTGTGCGAG 2136
Db 741 PheGlnArgPheArgGlnGlnLysGlnAlaArgLeuAlaGlnGlnGlnGlnGlnGlnGln 760
OY 2137 GTTGAC-----ACCAGCTCCCTGAGCGCGGAGCAAT 2166
Db 761 LeuAspAspLeuAspValGlnLysGlyAsnAlaLeuThrAspHisThrSerAlaAsnHis 780
OY 2167 ACCCTATG-----TCCAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 781 SerLeuValLysAlaSerValValThrValArgLysSer----- 793

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OY 2221 GTCTCCCGAGCGCCAGTGTATGAGCCCTCCAGCGCCCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 794 -----ProIleThrProValSerPheGlnAlaIleAlaIleThr 805
OY 2281 TCA-----TCTCAGCTGCGCAAGCTG-----CTATCCCGAGCT 2313
Db 806 SerThrMetSerAspHisAlaLysIleHisAlaProGlySerGlnCysLeuGlnProLys 825
OY 2314 CGAACACGA-----CCCGGCTGCTAGT-----GGC 2343
Db 826 AlaValSerCysAspProAlaLysAlaGlyGlyTyrAlaArgPheLysAspAlaCysGly 845
OY 2344 AGAGAGAGCGCAGCAGCGCGCGGCTTGTGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2403
Db 846 LysGlyGlnAspTyrAsnLys--ValSerLysAlaGlnSerMetGlnThrLeuProGln 864
OY 2404 CGGCGCCCTGAGAGGGGTACGGCTGCGCCCGCATGCGCATGAGATGTGCCCGCAGCTGAGC 2463
Db 865 ArgThr-----LysAlaProGlnGlnAlaThr 873
OY 2464 CCCAGGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2523
Db 874 LeuLysLysThr-----AspSerCysAspSerGlyIleThrLysSerAspLeu 889
OY 2524 CGCGTGGCGCAGTGTGCGCGCGGATGTAGACAGCAGCCCTCCCTGAGCAGAGAGCGGC 2583
Db 890 ArgLeuAspAsnValGly-----GlnThrAlaGlySerProGlnAspArgSerPro 905
OY 2584 CTGCTCACT-----GTGCCCATGAGCGCCAGCAGGAGCAGCAGG 2619
Db 906 IleLeuAlaGlnValLysHisSerPheTyrProIleProGlnGlnThrLeuGlnAlaThr 925
OY 2620 AACACAGACACATGACAACTTCCGAGCGGCTGACAGAGCTGTGACAGCAGAGTGTCTTTC 2679
Db 926 ValLeuGlnValLysTyrGlnLeuLysGlnLysPheLysAlaLeuAsnAlaLysMetThr 945
OY 2680 CAGATGCGGAGAGAGTGCAGATCACTTCCGAGCGCTGTGACAGCTTGTCTGCGCGCCAC 2739
Db 946 SerIleGlnLysGlnLeuSerGlnIleLeuArg-----IleLeuMetSerArg 961
OY 2740 AGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2790
Db 962 GlySerAlaGlnSerProGlnGlnThrGlnIleLysAlaArgProGlnSer 978

```

RESULT 9  
T42394

potassium channel protein eag homolog - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T42394  
R:Waterston, R.  
submitted to the EMBL Data Library, June 1999  
A:Reference number: 222153  
A:Accession: T42394  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-934 <WAT>  
A:Cross-references: EMBL:AF036695; PIDN:AMB88348.1  
C:Genetics:  
A:Introns: 27/1; 66/2; 104/1; 147/1; 164/3; 222/2; 263/3; 301/3; 410/1; 468/2; 667/3;  
A:Note: F16B3.1

Alignment Scores:  
Pred. No.: 9.86e-58  
Score: 1257.00  
Percent Similarity: 48.09%  
Best Local Similarity: 31.31%  
Query Match: 20.64%  
DB: 2  
Gaps: 33

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x T42394 (1-934)

[illegible]

```
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_rev10n 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T19579
R:Mortimore, B.
submitted to the EMBL Data Library, August 1994
A.Reference number: Z19145
A.Accession: T19579
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-514 <MUL>
A.Cross-references: EMBL:Z35596; PIDN:CAA84644.1; GSPDB:GN00021; CESP:C3OD11.1
A.Experimental source: clone C3OD11
C.Genetics:
A.Gene: CESP:C3OD11.1
A.Map position: 3
A.Introns: 49/3; 77/2; 151/3; 192/3; 244/2; 264/1; 366/3; 435/2; 479/1

Alignment Scores:
Pred. NO.:          5,79e-46
Score:              1029.50
Percent Similarity: 61.78%
Best Local Similarity: 44.42%
Query Match:        16.91%
Db:                 2
Gaps:               10

US-09-965-830-L_COPY_6_3257 (1-3252) x T19579 (1-514)
QY 604 TTGCCTGAGTACAAAGTAGCCGCCATCGGGGAAGTCGCCCTTCATCCTTGACACTGTGG 663
    |||||.....:|||||
Dd 58 LeuproguturlyrlslenglnprontharglleHLSHCystHrilleAlHlsryser 77
    ::::|
QY 664 GCACTGAGAGCCACTGGGATGGCTTCATCCTGCTGCGCCACACTATAGTGGCTACT 723
    :|||:|||||
Dd 78 ProPhelysalvalatTPasPTripelleleuleuleuValileTyThralavalphe 97
    :|||:|||||
QY 724 GTGCCCTACACAGCTGTGTGTGAGCACAGCAGGGAG-----CCAGT 765
    ||| |
Dd 98 ThProtyr--ValAlalaphelLeuleuArgluleuInaspThralalySer 116
    ||| |
QY 766 GCCGCCGCCGCCGCCACCACGCTGTGACCTGGCCGTGGAGGTCCTTCATCCTGAC 825
    ||| :|||
Dd 117 ArgPheThrIupProleugluilleValaspleulleValasplemetPellevalasp 136
    :|||:|||||
QY 826 ATTGCTGTAATTCCGTACCATTCGTGTCCAAGTCGGGC-----CAGTGTGTG 876
    |||:|||||
Dd 137 IlellellensmPheArtylrThrTyValasnglunsmaspGlualacysglnValval 156
    :|||:|||||
QY 877 TTTGCCCAAGATCCATTTCCTCACTACGTACACACCGCTGTCCTGCTGATGTGCATC 936
    ||| |||
Dd 157 SerAspProglyllysIlelatnrHlsTyRphelysglTYRphellelleasPmetVal 176
    |||
QY 937 GCAGCGCTGCCCTTGACCTGCTA-----CATGCCCTCAAGGTCAACGTGTAC 984
    |||||:|||||
Dd 177 AlaAlavalProPheaspLeuleuleuValSerThasSeraspIunhrThrThrlen 196
    :|||:|||||
QY 985 TTCGGGGCCANCTGCTGAGAAGCGGTGCGCTGTGCGCTGCGCTGCGCTGCGCGG 1044
    |||
Dd 197 Ilegly-----LeuleulysThralaryleuleuArgyleuValargyalaarglys 214
    |||
QY 1045 CTGGACCGGTACTGCGCATGACAGCGCCGTGTGCTGACACTGCTCATGGCCGTGTGGC 1104
    |||||:|||||
Dd 215 LeuasparyTyrsErglutyrIlglylaAlavalLeuleuleuMetAlathrpheala 234
    |||||:|||||
QY 1105 CTGCTCGGCACTGGSGTGCGCTGCTGTGATTACATGCAATGGCCAGCGGAGATCGAGAGC 1164
    |||||:|||||
Dd 235 LeuillealahstIrrleualacysIlerpyralalegylSeralagIudenserIs 254
    |||||:|||||
QY 1165 AGCGAATCCGAGCTGCCGATGGCTGGCGGTGCGAGGAGCTGGCCCCGCGAGTGGAGACT 1224
    |||
Dd 255 Lys-----GluTyrrThrThrleuhsgInleuSerlysgInleualaeln 269
    |||||
QY 1225 CCTACTACCTGCTGTGGCGCGGAGGCCAGCTGAGGGAACAACACTCCGCCAGATGACAC 1284
    |||||
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[illegible]

RESULT 12  
I50630  
alpha subunit of cone photoreceptor CNG-channel - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_rev10n 13-Sep-1996 #ext\_change 13-Aug-1999  
C:Accession: I50630  
C:Bonick, W.; Altenhofen, W.; Muller, F.; Dore, R.

Neuron 10, 865-877, 1993  
A>Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated chan  
A:Reference number: I50630; MUID:93264082; PMID:7684334  
A:Accession: I50630  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-735 <BON>  
C:Cross-References: EMBL:x89598; NID:g908850; PID:CA61757.1; PID:g908851  
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleot  
E:524-648/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <C

Alignment Scores:  
Pred. No.: 1.43e-14 Length: 735  
Score: 423.50 Matches: 149  
Percent Similarity: 40.74% Conservative: 115  
Best Local Similarity: 22.99% Mismatch: 224  
Query Match: 6.96% Indels: 160  
DB: 2 Gaps: 22

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x I50630 (1-735)

[illegible]









Thu May 8 08:49:43 2003

us-09-965-830-1\_copy\_6\_3257.rpt

Page 23

Db 301 phearYIIleolYasnlleuValleuYrIIleleu ----- Iellellehs 315

QY 1117 TGGGTGGCCGCGCTCGTGGTTTACATTGGCCAGGAGATCGAGACGCAATCCAG 1177

Db 316 TTPasnlacysIIleYrPhealIleSerIys ----- 326

QY 1177 CTGCTCGAATGGTGGCGTGCAGAGAGCTGGCCCGCCACCTGGAATCTCCACTACCTG 1230

Db 327 -----PheIIleolYpHe ----- 330

QY 1237 GTGGGCGGAGGCGCAGCTGGAGGGAACAGCTCGGGCCAGAGTGAACACTGCAGACAGC 1296

Db 331 ----- glythrAspSerTrpValYrProasnlleSerIlePro 343

QY 1297 ACCGAGGCCAAGCGGAGCGGGCTGGAGCTGTGGCGGCCGTGCGCCAGCGCCATC 1356

Db 344 GIuHISglYatg-----LeuSerArIglYstrY 352

QY 1357 ATGACCTCCCTCTACTCTGCACCTACAGACCTTCACAGCTGGCGTTGGCAGAGTGC 1416

Db 353 IIleYrSerIleuYrTrpSerThrIleuhrIleuhrIIleglY--GIuThrProPro 371

QY 1417 GCCACACGAGACCGGACAAGACTCTTCTGCATCTGCACCATGCTCATGCGGCCCTGATG 1476

Db 372 ProvalIysAspIgluGIuTrYleuPheValValalAspPheIleuValGIYalIleuIle 391

QY 1477 CACGCGGGGTGTGGGAAGCTGACAGCGCCATCATCCAGCGCATGTACGCGCGCTTT 1536

Db 392 PhealIarhrIleValIGIYasnlValIGIYSerMetIleSerasnlmetAsnlaserArIalA 411

QY 1537 CTGTACCAACAGCCGCGAGCGGACCTCGGCACATCCGATCCGACACCCGATCCCAAG 1596

Db 412 GIuHeglnalIatYsIIleAspSerIleYsGlnIYmetGIuPhearIglYsValIhrIys 431

QY 1597 CCGCTTCAAGACGCGCATGCTGAGTACTCTCAGGCGCCACMCGCGCGGAGAACATGGCATC 1656

Db 432 AspIeulIuhrArIglValIIleArIgtTrpPheAspTrYleuTrpIlaAsnlYsIYthrVal 451

QY 1657 GACACCAACGAGCTGTGTGACAGACCTCCCTGACGAGCTGGCGGCGACAGATCGGCATGAC 1716

Db 452 AspGIuIYsgIuValIleuIYsSerIleuProAspIYsIleuIYsIlaGluIlealIleAs 471

QY 1717 CTGCAACAGAGGTCTCTG--CAGCTGCCACTGTGTGAGCGGCGCACGCGCGCTGCTG 1773

Db 472 ValHISleuAspIhrIleuIYsIYsValArIglIlePheGlnAspCysIuIlaGlyIleuIle 491

QY 1774 CGGGCACTGTCTGTGGCCCTGCGCGCCCGCGCTCTGTGCAGCCGCGGAGTACCTATCCAC 1833

Db 492 ValGIuIleuValIleuIYsIleuArIgtProIhrValPheSerTrpGIYasprIleCysIYs 511

QY 1834 CAGGCGATGACCTGTGAGGCCCTCTACTTGTCTGTCTGTGCTCCATGAGAGGTGTC-- 1890

Db 512 IYsgIYAspIleolYIYsgIuIuethYrIIleAsnGIuGIYIYsIleuIlaValIalA 531

QY 1891 ---AAGGTGTGCACCGCTGTCCGCATCCATGAGGAGGCGGACCTGATGGC----- 1938

Db 532 AspAspGIYalIhrIlePheValIValIleuSerAspGIYSerTrpPheolYIuIleSer 551

QY 1939 ---TGTGACTGTCGCCCGCGGAGAGAGGTGAAGGCCAATGCCAGCTGAGAGGCTG 1995

Db 552 IleIeuAsnlleIYglYSerIYsSerIglYasnlArIgtArIhrAlaAsnlleArIserIle 571

QY 1996 ACGTACTGCGTCTGCAAGTGTGTGCAGCTGGCTGCGCTGCACAGACAGCTTGGCGGTGAC 2055

Db 572 GIYTrYserAspIleuPheCysIeulSerIYsAspIleuIuethGIuIlaIleuhrIglYrY 591

QY 2056 CCGGAGTTCGCCCGCGCTTCAGTCTGTGCGCTCCGAGGGAGACTACACTGAGGT 2115

Db 592 ProGIYglnAlIatYIys----- 597

QY 2116 GCTGGGGAGGCTGTGAGAGGTGACACCAAGCTTCCTGAGCGGCGCAATATCCCTTATG 2175

Db	598	-----AlaLeuGluGluIuLysGlyIaArgGlnIleLeuMetLysAspAsnLeuIleAsp	614
QY	2176	TCACGCTGGAGGAGAAAGACACAAATGGGGAGCAGGGCCCAAGCTCTCCACGCCCA	223
Db	615	GluGluLeuAlaIaArgIaGlyAlaAsp-----ProLysAsp	626
QY	2236	GCTGATGACCCCTCCAGCCCTCGCTGCTCCCTGGCTGCACCTTCATCCCTGAGTGGC	229
		:::	
Db	637	LeuGluGluIuLysValIuGluGlnLeuGlySerSerLeuAspThrLeuGlnThrIaArgPheAla	646
QY	2286	AAGTCGCAATCCCAACGCTCGAACGACCC-----CGGCTCGTCGA-----	233
		:::     :::	
Db	647	ArgLeuLeuAlaGluIuTrpAsnAlaThrGlnMetLysMetLysAspIaArgLeuSerGlnLeu	666
QY	2338	-----GGTGGCACAAGGAGGCCACGACAGGGCAGGGCTTGAAGCGTGAG	238
Db	667	GluSerGlnValLysGlyGlyIaAspLysProLeuAlaAspPolYolValIaProGlyAsp	686
		:::	
QY	2383	GCT 2385	
Db	687	Ala 687	

Search completed: May 7, 2003, 15:24:20  
Job time : 186 secs

